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Sequence Listing was accepted with existing errors.
See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: Wed Jun 13 13:10:08 EDT 2007

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Application No: 10797262 Version No: 2.1

Input Set:

Output Set:

Started: 2007-06-13 13:09:59.493
Finished: 2007-06-13 13:10:00.325
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 832 ms
Total Warnings: 9
Total Errors: 1
No. of SeqIDs Defined: 11
Actual SeqID Count: 11

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W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (8)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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SEQUENCE LISTING

<110> East Tennessee State University Research Foundation
Lampson, Bert
Velore, Jashree

<120> RNA-DEPENDENT DNA POLYMERASE FROM GEOBACILLUS STEAROTHERMOPHILUS

<130> 2826067.000002

<140> 10/797,262

<141> 2004-03-10

<160> 11

<170> PatentIn version 3.3

<210> 1

<211> 1263

<212> DNA

<213> Geobacillus stearothermophilus

<220>

<221> CDS

<222> (1)..(1263)

<400> 1

atg gct ttg ttg gaa cgc atc tta gcg aga gac aac ctc atc acg gcg 48
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1 5 10 15

ctc aaa cgg gtc gaa gcc aac caa gga gca ccg gga atc gac gga gta 96
Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val
20 25 30

tca acc gat caa ctc cgt gat tac atc cgc gct cac tgg agc acg atc 144
Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile
35 40 45

cgc gcc caa ctc ttg gcg gga acc tac ccg ccg gct gtc cgc agg 192
Arg Ala Gln Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg
50 55 60

gtc gga atc ccg aaa ccg ggc ggc aca ccg cag cta ggc att ccc 240
Val Gly Ile Pro Lys Pro Gly Gly Thr Arg Gln Leu Gly Ile Pro
65 70 75 80

acc gtg gtg gac ccg ctg atc caa caa gcc att ctt caa gaa ctc aca 288
Thr Val Val Asp Arg Leu Ile Gln Ala Ile Leu Gln Glu Leu Thr
85 90 95

ccc att ttc gat cca gac ttc tcc cct tcc agc ttc gga ttc cgt ccg 336
Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro
100 105 110

ggc cgt aac gcc cac gat gcc gtg ccg caa gcg caa ggc tac atc cag 384

Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln			
115	120	125	
gaa ggg tat cgg tac gtg gtc gac atg gac ctg gaa aag ttc ttt gat			432
Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp			
130	135	140	
cgg gtc aac cat gac atc ttg atg agt cgg gtg gcc cga aaa gtc aag			480
Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg Lys Val Lys			
145	150	155	160
gat aaa cgc gtg ctg aaa ctg atc cgt gcc tac ctg caa gcc ggc gtt			528
Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln Ala Gly Val			
165	170	175	
atg atc gaa ggg gtg aag gtg cag acg gag gaa ggg acg ccg caa ggc			576
Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr Pro Gln Gly			
180	185	190	
ggc ccc ctc agc ccc ctg ctg gcg aac atc ctt ctc gac gat tta gac			624
Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp			
195	200	205	
aag gaa ttg gag aag cga gga ttg aaa ttc tgc cgt tac gca gat gac			672
Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr Ala Asp Asp			
210	215	220	
tgc aac atc tat gtg aaa agt ctg cgg gca gga caa cgg gtg aaa caa			720
Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln			
225	230	235	240
agc atc caa cgg ttc ttg gag aaa acg ctc aaa ctc aaa gta aac gag			768
Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu			
245	250	255	
gag aaa agt gcg gtg gac cgc ccg tgg aaa cgg gcc ttt ctg ggg ttt			816
Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe			
260	265	270	
agc ttc aca ccg gaa cga aaa gcg cga atc cgg ctc gcc cca agg tcg			864
Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala Pro Arg Ser			
275	280	285	
att caa cgt ctg aaa cag cgg att cga cag ctg acc aac cca aac tgg			912
Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp			
290	295	300	
agc ata tcg atg cca gaa cga att cat cgc gtc aat caa tac gtc atg			960
Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met			
305	310	315	320
gga tgg atc ggg tat ttt cgg ctc gtc gaa acc ccg tct gtc ctt cag			1008
Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser Val Leu Gln			
325	330	335	
acc atc gaa gga tgg att cgg agg agg ctt cga ctc tgt caa tgg ctt			1056
Thr Ile Glu Gly Trp Ile Arg Arg Leu Arg Leu Cys Gln Trp Leu			

340

345

350

caa tgg aaa cgg gtc aga acc aga atc cgt gag tta aga gcg ctg ggg
 Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly
 355 360 365

ctg aaa gag aca gca gtg atg gag atc gcc aat acc cga aaa gga gct
 Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala
 370 375 380

tgg cga aca acg aaa acg ccg caa ctc cac cag gcc ctg ggc aaa acc
 Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr
 385 390 395 400

tac tgg acc gct caa ggg ctc aag agt ttg acg caa cga tat ttc gaa
 Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu
 405 410 415

ctc cgt caa ggt tga
 Leu Arg Gln Gly
 420

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<211> 420
<212> PRT
<213> Geobacillus stearothermophilus

<400> 2

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Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val
 20 25 30

Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile
 35 40 45

Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg
 50 55 60

Val Gly Ile Pro Lys Pro Gly Gly Thr Arg Gln Leu Gly Ile Pro
 65 70 75 80

Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr
 85 90 95

Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro
 100 105 110

Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln
115 120 125

Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp
130 135 140

Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg Lys Val Lys
145 150 155 160

Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln Ala Gly Val
165 170 175

Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr Pro Gln Gly
180 185 190

Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp
195 200 205

Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr Ala Asp Asp
210 215 220

Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln
225 230 235 240

Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu
245 250 255

Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe
260 265 270

Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala Pro Arg Ser
275 280 285

Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp
290 295 300

Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met
305 310 315 320

Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser Val Leu Gln
325 330 335

Thr Ile Glu Gly Trp Ile Arg Arg Leu Arg Leu Cys Gln Trp Leu
340 345 350

Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly
355 360 365

Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala
370 375 380

Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr
385 390 395 400

Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu
405 410 415

Leu Arg Gln Gly
420

<210> 3
<211> 1370
<212> DNA
<213> Artificial

<220>
<223> Plasmid construct

<220>
<221> misc_feature
<222> (1)..(1370)

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atatgcggca agacctgaat ctcatcccgc ggaaggagaa gatcacgtg gctttgttgg 120
aacgcacatctt agcgagagac aacctcatca cggcgctcaa acgggtcgaa gccaaaccaag 180
gagcaccggg aatcgacgga gtatcaaccg atcaactccg tgattacatc cgcgctcact 240
ggagcacgat ccgcgccaa ctcttggcgg gaacctaccg gccggcgct gtccgcagg 300
tcggaatccc gaaaccgggc ggccggcacac ggcagctagg cattcccacc gtggtgacc 360
ggctgatcca acaaggcatt cttcaagaac tcacacccat ttccgatcca gacttctccc 420
cttccagctt cggattccgt ccggggccgta acgcccacga tgccgtcgg caagcgcaag 480
gctacatcca ggaagggtat cggtaacgtgg tcgacatgga cctggaaaag ttctttgatc 540

gggtcaacca tgacatcttg atgagtcggg tggcccgaaa agtcaaggat aaacgcgtgc 600
tgaaaactgat ccgtgcctac ctgcaagccg gcgttatgat cgaaggggtg aaggtgcaga 660
cggaggaagg gacgcccggaa ggccccccc tcagccccct gctggcgaac atccttctcg 720
acgatttaga caaggaattg gagaagcgag gattgaaatt ctgccgttac gcagatgact 780
gcaacatcta tgtgaaaagt ctgcgggcag gacaacgggt gaaacaaagc atccaacgg 840
tcttggagaa aacgctcaaa ctcaaagtaa acgaggagaa aagtgcggtg gaccgcccgt 900
ggaaacgggc ctttctgggg tttagcttca caccggaacg aaaagcgcgatccggctcg 960
ccccaaaggc gattcaacgt ctgaaacagc ggattcgaca gctgaccaac ccaaactgga 1020
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attttcggct cgtcgaaacc ccgtctgtcc tttagaccat cgaaggatgg attcggagga 1140
ggcttcgact ctgtcaatgg ctcaatgg aacgggtcag aaccagaatc cgtgagttaa 1200
gagcgctggg gctgaaagag acagcggtga tggagatcgc caatacccgaaaggagctt 1260
ggcgaacaac gaaaacgccc caactccacc aggcctggg caaaacctac tggaccgctc 1320
aagggtcaaa gagtttgacg caacgatatt tcgaactccg tcaagggttga 1370

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<211> 32

<212> DNA

<213> Artificial

<220>

<223> Nucleotide primer containing NdeI restriction site

<220>

<221> primer_bind

<222> (1)..(32)

<400> 4

agacaacata tgccgcaaga cctgaatctc at 32

<210> 5

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Nucleotide primer containing BamHI restriction site

<400> 5

aatggatccg ctggcgaaca tccttctc 28

<210> 6
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Nucleotide primer containing PstI restriction site

<220>
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<222> (1)..(29)

<400> 6
attactgcag agcggtccag taggtttg 29

<210> 7
<211> 31
<212> DNA
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<223> Nucleotide primer containing HindIII restriction site

<220>
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<222> (1)..(31)

<400> 7
actcaagctt gagaagggtc tgacgttcat g 31

<210> 8
<211> 455
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of fusion protein

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<222> (1)..(455)

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<221> PEPTIDE
<222> (1)..(455)

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Arg Gly Ser His Met Arg Gln Asp Leu Asn Leu Ile Pro Arg Lys Glu
20 25 30

Lys Ile Thr Met Ala Leu Leu Glu Arg Ile Leu Ala Arg Asp Asn Leu
35 40 45

Ile Thr Ala Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile
50 55 60

Asp Gly Val Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp
65 70 75 80

Ser Thr Ile Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro
85 90 95

Val Arg Arg Val Gly Ile Pro Lys Pro Gly Gly Thr Arg Gln Leu
100 105 110

Gly Ile Pro Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln
115 120 125

Glu Leu Thr Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly
130 135 140

Phe Arg Pro Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly
145 150 155 160

Tyr Ile Gln Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys
165 170 175

Phe Phe Asp Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg
180 185 190

Lys Val Lys Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln
195 200 205

Ala Gly Val Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr
210 215 220

Pro Gln Gly Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp
225 230 235 240

Asp Leu Asp Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr
245 250 255

Ala Asp Asp Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg
260 265 270

Val Lys Gln Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys
275 280 285

Val Asn Glu Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe
290 295 300

Leu Gly Phe Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala
305 310 315 320

Pro Arg Ser Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn
325 330 335

Pro Asn Trp Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln
340 345 350

Tyr Val Met Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser
355 360 365

Val Leu Gln Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys
370 375 380

Gln Trp Leu Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg
385 390 395 400

Ala Leu Gly Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg
405 410 415

Lys Gly Ala Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu
420 425 430

Gly Lys Thr Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg
435 440 445

Tyr Phe Glu Leu Arg Gln Gly
450 455

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<222> (1)..(25)

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<213> Artificial

<220>
<223> Primer sequence

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<222> (1)..(25)

<400> 10
tcaaacactgt acggcacccg cattc 25

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<213> Artificial

<220>
<223> Primer sequence

<220>
<221> prim_transcript
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